



## SEQUENCE LISTING

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<120> MORPHOGENIC PROTEIN-SPECIFIC CELL SURFACE RECEPTORS AND USES THEREFOR

<130> CIBT-P04-543

<140> 09/982,543

<141> 2001-10-18

<150> 08/448,371

<151> 1995-06-02

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<170> PatentIn version 3.1

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Trp Phe Arg Glu Thr 275 Glu Ile Tyr Gln Thr 280 Val Leu Met Arg His Glu 285	
aac ata ctt ggt ttc ata gcg gca gac att aaa ggt aca ggt tcc tgg	1215
Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp	
290 295 300	
act cag ctc tat ttg att act gat tac cat gaa aat gga tct ctc tat	1263
Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr	
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Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu	
320 325 330	
gct tat tca gct gcc tgt ggt ctg tgc cac ctg cac aca gaa att tat	1359
Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr	
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ggc acc caa gga aag ccc gca att gct cat cga gac cta aag agc aaa	1407
Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys	
355 360 365	
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Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly	
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ctt gct gtt aaa ttc aac agt gac aca aat gaa gtt gat gtg ccc ttg	1503
Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu	
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Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp	
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gaa agc ctg aac aaa aac cac ttc cag ccc tac atc atg gct gac atc	1599
Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile	
415 420 425 430	
tac agc ttc ggc cta atc att tgg gag atg gct cgt cgt tgt atc aca	1647
Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr	
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gga ggg atc gtg gaa gaa tac caa ttg cca tat tac aac atg gta ccg	1695
Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro	
450 455 460	
agt gat ccg tca tac gaa gat atg cgt gag gtt gtg tgt gtc aaa cgt	1743
Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg	
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ttg cgg cca att gtg tct aat cgg tgg aac agt gat gaa tgt cta cga	1791
Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg	
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gca gtt ttg aag cta atg tca gaa tgc tgg gcc cac aat cca gcc tcc 1839  
Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser  
495 500 505 510

aga ctc aca gca ttg aga att aag aag acg ctt gcc aag atg gtt gaa 1887  
Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu  
515 520 525

tcc caa gat gta aaa atc tga tgggttaaacc atcggaggag aaactctaga 1938  
Ser Gln Asp Val Lys Ile  
530

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Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu Asn Gly Val  
35 40 45  
Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser  
50 55 60

Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly	65	70	75	80
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	85	90	95	
Ala	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp	100	105	110	
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn	115	120	125	
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly	130	135	140	
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Leu	Leu	Ile	Ser	Met	145	150	155	160
Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr	165	170	175	
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	Asn	Arg	Asp	180	185	190	
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp	195	200	205	
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	210	215	220	
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val	225	230	235	240
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu	245	250	255	
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	260	265	270	
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	275	280	285	
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln	290	295	300	
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe	305	310	315	320
Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr	325	330	335	
Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr	340	345	350	
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	355	360	365	
Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	370	375	380	
Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Val	Pro	Leu	Asn	Thr	385	390	395	400

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser  
 405 410 415  
 Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser  
 420 425 430  
 Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly  
 435 440 445  
 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp  
 450 455 460  
 Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg  
 465 470 475 480  
 Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val  
 485 490 495  
 Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu  
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 515 520 525  
 Asp Val Lys Ile  
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 aagagagcaa acaaaaagtt aaaggagcaa cccggccata agtgaagaga gaagtttatt 180  
 gataac atg ctc tta cga agc tct gga aaa tta aat gtg ggc acc aag 228  
 Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys  
 1 5 10  
 aag gag gat gga gag agt aca gcc ccc acc cct cgg ccc aag atc cta 276  
 Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu  
 15 20 25 30  
 cgt tgt aaa tgc cac cac cac tgt ccg gaa gac tca gtc aac aat atc 324  
 Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile  
 35 40 45  
 tgc agc aca gat ggg tac tgc ttc acg atg ata gaa gaa gat gac tct 372  
 Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser  
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 gga atg cct gtt gtc acc tct gga tgt cta gga cta gaa ggg tca gat 420  
 Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp

65	70	75	
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tgc tgc aca gaa agg aat gag tgt aat aaa gac ctc cac ccc act ctg Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu 95 100 105 110			516
cct cct ctc aag gac aga gat ttt gtt gat ggg ccc ata cac cac aag Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys 115 120 125			564
gcc ttg ctt atc tct gtg act gtc tgt agt tta ctc ttg gtc ctc att Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile 130 135 140			612
att tta ttc tgt tac ttc agg tat aaa aga caa gaa gcc cga cct cgg Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg 145 150 155			660
tac agc att ggg ctg gag cag gac gag aca tac att cct cct gga gag Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu 160 165 170			708
tcc ctg aga gac ttg atc gag cag tct cag agc tcg gga agt gga tca Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser 175 180 185 190			756
ggc ctc cct ctg ctg gtc caa agg aca ata gct aag caa att cag atg Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met 195 200 205			804
gtg aag cag att gga aaa ggc cgc tat ggc gag gtg tgg atg gga aag Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys 210 215 220			852
tgg cgt gga gaa aag gtg gct gtg aaa gtg ttc ttc acc acg gag gaa Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu 225 230 235			900
gcc agc tgg ttc cga gag act gag ata tat cag acg gtc ctg atg cgg Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg 240 245 250			948
cat gag aat att ctg ggg ttc att gct gca gat atc aaa ggg act ggg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly 255 260 265 270			996
tcc tgg act cag ttg tac ctc atc aca gac tat cat gaa aac ggc tcc Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser 275 280 285			1044
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aag cta gcc tac tcc tct gtc agc ggc cta tgc cat tta cac acg gaa Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu 305 310 315			1140
atc ttt agc act caa ggc aag cca gca atc gcc cat cga gac ttg aaa			1188

Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys	
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agt aaa aac atc ctg gtg aag aaa aat gga act tgc tgc ata gca gac	1236
Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp	
335 340 345 350	
ctg ggc ttg gct gtc aag ttc att agt gac aca aat gag gtt gac atc	1284
Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile	
355 360 365	
cca ccc aac acc cgg gtt ggc acc aag cgc tat atg cct cca gaa gtg	1332
Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val	
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ctg gac gag agc ttg aat aga aac cat ttc cag tcc tac att atg gct	1380
Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala	
385 390 395	
gac atg tac agc ttt gga ctc atc ctc tgg gag att gca agg aga tgt	1428
Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys	
400 405 410	
gtt tct gga ggt ata gtg gaa gaa tac cag ctt ccc tat cac gac ctg	1476
Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu	
415 420 425 430	
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Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met	
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aag aag tta cgg cct tca ttc ccc aat cga tgg agc agt gat gag tgt	1572
Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys	
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ctc agg cag atg ggg aag ctt atg aca gag tgc tgg gcg cag aat cct	1620
Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro	
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gcc tcc agg ctg acg gcc ctg aga gtt aag aaa acc ctt gcc aaa atg	1668
Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met	
480 485 490	
tca gag tcc cag gac att aaa ctc tga cgtcagatac ttgtggacag	1715
Ser Glu Ser Gln Asp Ile Lys Leu	
495 500	
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gagttcagac tttcctggaa gagagcacgg tgggcagaca cagaggaacc cagaaacacg	1835
gattcatcat ggctttctga ggaggagaaa ctgtttgggt aacttggtca agatatgatg	1895
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Asp	Gly	Glu	Ser	Thr	Ala	Pro	Thr	Pro	Arg	Pro	Lys	Ile	Leu	Arg	Cys	20	25	30
Lys	Cys	His	His	His	Cys	Pro	Glu	Asp	Ser	Val	Asn	Asn	Ile	Cys	Ser	35	40	45
Thr	Asp	Gly	Tyr	Cys	Phe	Thr	Met	Ile	Glu	Glu	Asp	Asp	Ser	Gly	Met	50	55	60
Pro	Val	Val	Thr	Ser	Gly	Cys	Leu	Gly	Leu	Glu	Gly	Ser	Asp	Phe	Gln	65	70	75
Cys	Arg	Asp	Thr	Pro	Ile	Pro	His	Gln	Arg	Arg	Ser	Ile	Glu	Cys	Cys	85	90	95
Thr	Glu	Arg	Asn	Glu	Cys	Asn	Lys	Asp	Leu	His	Pro	Thr	Leu	Pro	Pro	100	105	110
Leu	Lys	Asp	Arg	Asp	Phe	Val	Asp	Gly	Pro	Ile	His	His	Lys	Ala	Leu	115	120	125
Leu	Ile	Ser	Val	Thr	Val	Cys	Ser	Leu	Leu	Leu	Val	Leu	Ile	Ile	Leu	130	135	140
Phe	Cys	Tyr	Phe	Arg	Tyr	Lys	Arg	Gln	Glu	Ala	Arg	Pro	Arg	Tyr	Ser	145	150	155
Ile	Gly	Leu	Glu	Gln	Asp	Glu	Thr	Tyr	Ile	Pro	Pro	Gly	Glu	Ser	Leu	165	170	175
Arg	Asp	Leu	Ile	Glu	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	180	185	190
Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Lys	195	200	205
Gln	Ile	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	210	215	220
Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	225	230	235
Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	245	250	255
Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	260	265	270
Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	275	280	285
Asp	Tyr	Leu	Lys	Ser	Thr	Thr	Leu	Asp	Ala	Lys	Ser	Met	Leu	Lys	Leu	290	295	300
Ala	Tyr	Ser	Ser	Val	Ser	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Phe	305	310	315
Ser	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	325	330	335
Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu	Gly	340	345	350

Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro  
 355 360 365  
 Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp  
 370 375 380  
 Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met  
 385 390 395 400  
 Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser  
 405 410 415  
 Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro  
 420 425 430  
 Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys  
 435 440 445  
 Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg  
 450 455 460  
 Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro Ala Ser  
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 Ser Gln Asp Ile Lys Leu  
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 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala  
 5 10 15  
 ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac 153  
 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn  
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 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg  
 40 45 50  
 cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc 249  
 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg  
 55 60 65  
 ccg cgc ccg cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg 297

Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met	
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Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly	
85 90 95	
ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc	393
Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly	
100 105 110 115	
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Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp	
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Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe	
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cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc	537
His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile	
150 155 160	
cca gaa ggc gaa gct gtc acg gca gcc gaa ttc cgg atc tac aag gac	585
Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
165 170 175	
tac atc cgg gaa cgc ttc gac aat gag acg ttc cgg atc agc gtt tat	633
Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr	
180 185 190 195	
cag gtg ctc cag gag cac ttg ggc agg gaa tcg gat ctc ttc ctg ctc	681
Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu	
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gac agc cgt acc ctc tgg gcc tcg gag gag ggc tgg ctg gtg ttt gac	729
Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp	
215 220 225	
atc aca gcc acc agc aac cac tgg gtg gtc aat ccg cgg cac aac ctg	777
Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu	
230 235 240	
ggc ctg cag ctc tcg gtg gag acg ctg gat ggc cag agc atc aac ccc	825
Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro	
245 250 255	
aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc	873
Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro	
260 265 270 275	
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Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile	
280 285 290	
cgg tcc acg ggg agc aaa cag cgc agc cag aac cgc tcc aag acg ccc	969
Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro	
295 300 305	
aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc	1017
Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser	
310 315 320	

agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc 1065  
 Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe  
 325 330 335

cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc 1113  
 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala  
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gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg 1161  
 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met  
 360 365 370

aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac 1209  
 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn  
 375 380 385

ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc 1257  
 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala  
 390 395 400

atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa 1305  
 Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys  
 405 410 415

tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac tagctcctcc 1351  
 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His  
 420 425 430

gagaattcag accctttggg gccaaagtttt tctggatcct ccattgctcg ccttggccag 1411

gaaccagcag accaactgcc ttttgtgaga cttccctc cctatcccca actttaag 1471

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gcataaagaa aaatggccgg gccaggtcat tggtgggaa gtctcagcca tgcacggact 1651

cgtttccaga ggtaattatg agcgctacc agccaggcca cccagccgtg ggaggaagg 1711

ggcgtggcaa ggggtgggca cattggtgtc tgtgcgaaag gaaaattgac ccggaagttc 1771

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Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser  
 35 40 45

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu  
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Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro  
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 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly  
 85 90 95  
 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser  
 100 105 110  
 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr  
 115 120 125  
 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys  
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 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu  
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 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile  
 165 170 175  
 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile  
 180 185 190  
 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu  
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 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu  
 210 215 220  
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg  
 225 230 235 240  
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser  
 245 250 255  
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn  
 260 265 270  
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe  
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 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser  
 290 295 300  
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu  
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 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn  
 355 360 365  
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 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln  
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Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
          35           40           45
Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
          50           55           60
Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
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Xaa Ala Cys Gly Cys His
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